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CLAIMS

What is claimed is:

- 09744055-03264  
00220-58044260
1. A method for controlling starch synthesis in tomatoes comprising:  
providing a population of plants derived from interspecific crosses of  
5 *Lycopersicon* spp. with *Lycopersicon esculentum* genotypes; and  
selecting individuals of said population that each contain an allele of a gene that  
increases starch synthesis, said gene originating from said *Lycopersicon* spp.
2. The method according to claim 1 wherein said step of selecting comprises  
selecting individuals that each contain the allele of the gene that encodes for an enzyme that  
10 catalyzes a metabolic step in starch synthesis.
3. The method according to claim 1 wherein said step of selecting comprises  
selecting individuals that each contain the allele of the gene that encodes for a subunit of  
ADPGPPase.
4. The method according to claim 1 wherein said step of selecting comprises  
15 selecting individuals that each contain the allele of the gene that encodes for a *Lycopersicon*  
*hirsutum*-derived subunit of ADPGPPase.
5. The method according to claim 1 wherein said step of selecting comprises  
selecting by using a molecular marker for said gene.
6. The method according to claim 5 wherein said molecular marker comprises step  
20 of selecting comprises a *Lycopersicon hirsutum*-derived large subunit (LS1) of ADPGPPase.
7. The method according to claim 2 wherein said step of selecting comprises  
selecting by measuring activity of said enzyme in young fruit and selecting those young fruit  
with high activity of said enzyme.
8. The method according to claim 2 wherein said step of selecting comprises  
25 selecting by measuring ADPGPPase activity of said young fruit, and selecting those young fruit  
with high ADPGPPase activity.
9. The method according to claim 1 wherein said *Lycopersicon* spp. comprises a  
*Lycopersicon* spp. of green-fruited *Eriopersicon* subgenus.
10. The method according to claim 1 wherein said *Lycopersicon* spp. comprises  
30 *Lycopersicon hirsutum*.
11. A method of producing genetically transformed plants which have elevated starch  
content, comprising the steps of:  
a) inserting into the genome of a plant cell a recombinant double stranded DNA

molecule comprising

(i) a selected promoter

(ii) a structural DNA sequence that causes the production of an RNA sequence

which encodes the above described ADPGPPase LS1 protein

5 b) obtaining transformed plant cells

c) regenerating from the transformed plant cells genetically transformed plants with elevated starch content.

12. The method according to claim 11 wherein said plant cell is selected from the group consisting of a tomato cell, a potato cell, a cell from a solanaceous plant, a legume cell, and a grain crop cell.

13. The method according to claim 11 wherein said promoter is selected from the group consisting of an immature fruit promoter, a tuber promoter, and a seed promoter.

14. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in an immature fruit.

15. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in a tuber.

16. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in a seed.

17. A method according to claim 1 and additionally comprising the step of propagating said individuals of said population.

18. A method according to claim 17 wherein the step of propagating includes the step of vegetative propagation.

19. A method according to claim 17 wherein the step of propagating includes the step of propagation by seed.

20. A method according to claim 11 and additionally comprising the step of propagating said genetically transformed plants.

21. A method according to claim 20 wherein the step of propagating includes the step of vegetative propagation.

22. A method according to claim 20 wherein the step of propagating includes the step of propagation by seed.

23. A plant produced according to the method of claim 1.

24. A plant produced according to the method of claim 11.

25. A fruit produced by a plant in accordance with claim 23.

26. A fruit produced by a plant in accordance with claim 24.

27. A seed which when grown yields a plant in accordance with claim 23.

28. A seed which when grown yields a plant in accordance with claim 24.

29. A gene that controls sucrose-starch metabolism comprising a nucleotide sequence as follows:

1 ATGAAATCGA CGGTTTCATTT GGGGAGAGTG AGCACTGGTG CTTTAACAA  
51 TGGAGAGAAG GAGATTTTTT GGGAGAAGAT GAGAGGGAGT TTGAACAACA  
101 ATCTCAGGAT TAATCAGTTG TCGAAAAGTT TGAAACTTGA GAAGAAGGAG  
151 AAGAAAGATTA AACCTGGGGT TGCTTACTCT GTGATCACTA CTGAAAATGA  
201 CACACAGACT GTGTTCGTAG ATATGCCACG TCTTGAGAGA CGCCGGGCAA  
251 ATCCCAAGGA TGTGGCTGCA GTCATATTAG GAGGAGGCGA AGGGACCAAG  
301 TTATTCCAC TTACAAGTAG AACTGCAACC CCTGCTGTTC CGGTTGGAGG  
351 ATGCTACAGG CTCATAGACA TCCCGATGAG CAACTGTATC AACAGTGCTA  
401 TTAACAAGAT TTTTGTGCTG ACACAGTACA ATTCTGCTGC CCTGAATCGT  
451 CACATTGCTC GAACGTATTT TGGCAATGGT GTGAGCTTTG GAGATGGATT  
501 TGTCGAGGTA CTAGCTGCAA CTCAGACACC TGGGGAAGCA GGAAAAAAT  
551 GGTTC AAGG AACAGCAGAT GCTGTCAGAA AATTTATATG GGTTCCTGAG  
601 GACGCTAAGA ACAAGAATAT TGAAAATATC CTTGTATTAT CTGGGGATCA  
651 TCTTTATAGG ATGGATTATA TGGAGTTGGT GCAGAACCAT ATTGACAGAA  
701 ATGCTGATAT TACTCTTTCA TGTGCACCAG CTGAGGACAG CCGAGCATCA  
751 GATTTTGGGC TGGTCAAGAT TGACAGCAGA GGCAGAGTTG TCCAGTTTGC  
801 TGAAAAACCA AAAGGTTTGT AGCTTAAAGC AATGCAAGTA GATACTACTC  
851 TTGTTGGATT ATCTCCAAGG GATGCGAAGA AATCCCCTTA TATTGCTTCA  
901 ATGGGAGTTT ATGTTTTCAA GACAGATGTA TTGCTGAAGC TCTTGAAATG  
951 GAGCTACCCC ACTTCTAATG ATTTTGGCTC TGAAATTATA CCAGCAGCTA  
1001 TTGATGATTA CAATGTCCAA GCATACATTT TCAAAGACTA TTGGGAGGAC  
1051 ATTGGAACAA TTAAATCTTT CTATAATGCT AGCTTGGCGC TCACACAAGA  
1101 GTTTCAGAG TTCCAATTTT ATGATCCAAA AACACCTTTT TACACATCTC  
1151 CTAGGTTTCT TCCACCAACC AAGATAGACA ATTGCAAGAT TAAGGATGCC  
1201 ATAATTTCTC ATGGATGTTT CTTGCGAGAT TGCTCTGTGG AACACTCCAT  
1251 AGTGGGTGAA AGATCACGCT TAGACTGTGG TGTGAACTG AAGGATACTT  
1301 TCATGATGGG AGCAGACTAC TACCAACAG AATCTGAGAT TGCCTCCCTG  
1351 TTAGCAGAGG GGAAAGTACC GATTGGGATT GGGGAAAATA CAAAAATAAG  
1401 GAAATGTATC ATTGACAAGA ACGCAAAGAT AGGAAAAAAT GTTTCATCA  
1451 TTAATAAAGA TGGTGTTC AA GAGGCAGACC GACCAGAGGA AGGATTCTAC  
1501 ATACGATCAG GGATAACCAT TATATCAGAG AAAGCCACAA TTAGAGATGG  
1551 AACAGTTATA TGA

30. A protein that controls sucrose-starch metabolism comprising a derived amino acid sequence as follows:

MKSTVHLGRVSTGGFNNGEKEIFGEKMRGSLNNNLRLINQL  
SKSLKLEKKEKKIKPGVAYSVITTENDTETVFVDMPLRERRAN  
PKDVA AAVILGGGEGTKLFPLTSRTATPAVPVGGCYRLIDIPMSNC  
INSAINKIFVLTQYNSAALNRHIARTYFGNGVSFGDGFVEVLAAT  
QTPGEAGKKWFQGTADAVRKFIWVFEDAKNKNIENILVLSGDHL  
YRMDYMELVQNHIDRNADITLSCAPAEDSRASDFGLVKIDSRGR

VVQFAEKPKGFELKAMQVDTTLVGLSPQDAKKSPYIASMGVYV  
FKTDVLLKLLKWSYPTSNDFGSEIIPAAIDYINVQAYIFKDYWED  
IGTIKSFYNASLALTQEFPEFQFYDPKTPFYTSRFLPPTKIDNCKI  
KDAIISHGCFLRDCSVELSIYGER SRLDCGVELKDTFMMGADYY  
5 QTESEIASLLAEGKVPIGIGENTKIRKCIIDKNAKIGKNVSIINKDG  
VQEADRPEEGFYIRSGITMISEKATIRDGTVI

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